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16 pcts

Lipid phosphate phosphatases and uses thereof for treating neuronal diseases

The present invention relates to lipid phosphate phosphatase proteins, genes coding for them, vectors and cells comprising them, antibodies directed against them, methods of identifying compounds binding to them and functional interactors as well as to the use of proteins, genes, vectors, cells, interacting compounds and functional interactors for treating neuronal diseases and/or injuries.

Axons in the central nervous system (CNS) elongate through the extracellular space over long distances (N. Tessier-Lavigne and C. S. Goodman (1996) Science 274:1123-1133). This occurs during development (C. S. Goodman (1996) Annu. Rev. Neurosci.19:341-377 and H. Super and E. Soriano (1994) J. Comp. Neurol. 344:101-120) and during axonal sprouting in response to partial deafferentation (C. Cotman et al. (1977) J. Neurocytol. 6:455-464 and M. Frotscher et al. (1997) Trends Neurosci. 20:218-223). The extracellular space, however, is an outgrowth repellent environment that allows axonal elongation only under specific molecular conditions (E. Stein and N. Tessier-Lavigne (2001) Science 291:1928-1938). Molecules involved in axonal outgrowth, such as semaphorins, netrins, or ephrins (S. A. Colamarino and M. Tessier-Lavigne (1995) Cell 81:621-629, H Kobayashi et al. (1997) J. Neurosci. 17:8339-8352, E. Stein et al. (1999) J. Neurosci. 19:8585-8893 and A. Steup et al. (2000) Mol. Cell Neurosci. 15:141-155) are able to transduce outgrowth promoting as well as inhibiting signals to elongating axons via specific receptors.

In the hippocampus, afferent connections from the entorhinal cortex enter in a layer-specific manner during development (T. Skutella and R. Nitsch (2001) Trends Neurosci. 24:107-113). This specific axonal navigation depends on molecular cues expressed along the pathway and in the target region (T. Skutella and R. Nitsch, *supra*). Transection of entorhinal axons in the adult leads to a specific deafferentation in the hippocampus with subsequent regenerative axon sprouting by remaining afferents into the denervated zones (C. Cotman et al, *supra* and D.A Matthews et al. (1976) Brain Res. 115:23-41). It has been shown that signaling via bioactive lipid phosphates such as phosphatidate (PA), lysophosphatidate (1- or 2-oleoyl-lysophosphatidic acid; LPA) or sphingosine-1-phosphate (S-1-P) are involved in cell migration, mitogenesis and neurite retraction (K. Jalink et al. (1994)

Biochim. Biophys. Acta 1198:185-196, W. H. Moolenaar (1995) Curr. Opin. Cell Biol. 7:203-210 and N. Zhang et al. (1997) Nature 385:64-67) and in particular it has been shown that signaling via extracellular LPA plays an important role in CNS development and that postmitotic neurons are at least one endogenous source for LPA in the nervous system (N. Fukushima et al. (2000) Dev. Biol. 228:6-18). LPA has properties of an extracellular neurite repellent factor (K. Jalink (1994) *supra* and K. Jalink et al. (1993) Cell Growth Differ. 4:247-255). It is present in the extracellular space of the nervous system (Fukushima et al. (2000) *supra* and J. Bothmer et al. (1992) Neurochem. Int. 21:223-228) and mediates diverse cellular responses through the activation of multiple signal transduction pathways (W. H. Moolenaar (1995) *supra*). One major structural effect of LPA on neurons is rapid neurite retraction with subsequent cell rounding. Therefore, LPA and similar bioactive lipid phosphatases inhibit a regrowth of axons following neuronal lesion. Therefore, it is a problem known in the art, that after neuronal damage due to, for example, neuronal disease or trauma a regrowth of axons does not occur.

Within the context of the present invention it has been found that the expression of a family of genes called plasticity-related genes (PRGs) overcomes the repellent effect of bioactive lipid phosphates, in particular of LPA and, thus, allows the regrowth of axons in spite of the presence of bioactive lipid phosphates. Therefore, the present invention is directed at an isolated protein comprising the same or substantially the same amino acid sequence selected from the group consisting of human PRG-1, human PRG-2, human PRG-3, human PRG-4, mouse PRG-1, mouse PRG-2, mouse PRG-3, mouse PRG-4, rat PRG-1, rat PRG-2, rat PRG-3, and rat PRG-4 (depicted in SEQ ID NOs: 1 to 12), respectively, or a splice variant or a salt thereof. A protein having substantially the same amino acid sequence comprises proteins with at least about 95%, preferably at least about 96%, more preferably at least about 97%, more preferably with at least about 98% and most preferably with at least about 99% amino acid sequence identity. The amino acid exchanges are preferably so called conservative changes meaning substitutions of, for example, a polar amino acid residue by another polar amino acid residue, of a acidic amino acid residue by another acidic amino acid residue or of a basic amino acid residue by another basic amino acid residue.

Proteins having substantially the same amino acid sequence within the meaning of this invention exhibit in a preferred embodiment lipid phosphate phosphatase activity The lipid

phosphate phosphatase activity of a given protein with substantially the same amino acid can be tested, for example, by the ectophosphatase assay described in example 11 below. The proteins employed in the assay can either be purified from cells or can be recombinantly expressed and purified by methods well known in the art.

In one embodiment of the present invention the protein comprises at least one fragment of the human PRG-1, PRG-2, PRG-3, and PRG-4 or mouse PRG-1, PRG-2, PRG-3 and PRG-4 or rat PRG-1, PRG-2, PRG-3 and PRG-4. A fragment within the meaning of the present invention refers to one of the proteins according to SEQ ID NOs: 1 to 12 bearing at least one N-terminal, C-terminal and/or internal deletion. The resulting fragment has a length of at least about 50, preferably of at least about 100, more preferably of at least about 150, more preferably of at least about 200, more preferably of at least about 250, more preferably of at least about 300 and in case of human PRG-1 and PRG-2 or mouse PRG-1 and PRG-2 or rat PRG-1 and rat PRG-2, more preferably of at least about 350 and most preferably of at least about 400 amino acids.

Preferably, the fragment is an N-terminal fragment which comprises 330 amino acids or less as outlined above, which are highly conserved between, for example, PRG-1 and members of the family of LPP membrane-associated phosphatic acid phosphatase ectoenzymes, which have six membrane spanning domains with their active site located on the external surface of the plasma membrane. This domain comprises preferably the catalytic region. For example, human PRG-1 carries a catalytic histidine at position 252, which is involved in the phosphatase activity of human PRG-1. Similarly human, mouse and rat PRG-3 comprises a domain highly homologous to human PRG-1, which in rat PRG-3 spans amino acids 210 to 212 and includes a histidine residue at amino acid 209. Therefore, in a preferred embodiment any N-terminal fragment of the proteins of the present invention comprises the catalytic site, preferably including the conserved His-residue. The fragment itself has preferably an amino acid sequence identity with hPRG-1, hPRG-2, hPRG-3, hPRG-4, mPRG-1, mPRG-2, mPRG-3, mPRG-4, rPRG-1, rPRG-2, rPRG-3, and rPRG-4, respectively, of at least about 95%, preferably of at least about 96%, more preferably of at least about 97%, more preferably of at least about 98%, more preferably of at least about 99% and most preferably of 100%.

The C-terminal cytoplasmatic part of the PRG proteins is potentially involved in regulation of lipid phosphate phosphatase activity and/or signaling and, thus, a further preferred fragment comprises a C-terminal fragment, which comprises about 413 amino acids or less as outlined above and which comprises regions required for above activity of the PRG proteins. The fragment itself has preferably an amino acid sequence identity with hPRG-1, hPRG-2, hPRG-3, hPRG-4, mPRG-1, mPRG-2, mPRG-3, mPRG-4, rPRG-1, rPRG-2, rPRG-3, and rPRG-4, respectively, of at least about 95%, preferably of at least about 96%, more preferably of at least about 97%, more preferably of at least about 98%, more preferably of at least about 99% and most preferably of 100%.

In a further aspect the present invention is directed at a nucleic acid, which comprises at least one nucleic acid encoding one of the proteins of the present invention. Preferably the nucleic acid consists of DNA or RNA, wherein the DNA preferentially is either single or double stranded. Also comprised are DNA's, which hybridize to one of the aforementioned DNA's preferably under stringent conditions like, for example, hybridization at 60°C in 2.5 x SSC buffer and several washes at 37°C at a lower buffer concentration like, for example, 0.5 x SSC buffer and which encode proteins exhibiting lipid phosphate phosphatase activity and/or association with plasma membranes. Additional reagents required for carrying out stringent Northern or Southern blots like, for example, single stranded salmon sperm DNA are well known in the art. Also comprised are nucleic acid sequences, which are related to the nucleic acids according to SEQ ID No. 13-24 and/or the hybridizing nucleic acids as outlined above by the degeneration of the genetic code.

In a preferred embodiment of the nucleic acid of the present invention the nucleic acid comprises a nucleic acid selected from the group consisting of the human PRG-1 gene, the human PRG-2 gene, the human PRG-3, the human PRG-4, the mouse PRG-1 gene, the mouse PRG-2 gene, the mouse PRG-3, the mouse PRG-4, the rat PRG-1, the rat PRG-2, the rat PRG-3, and the rat PRG-4 gene (see SEQ ID NOs: 13 to 24).

In a further embodiment the nucleic acid of the present invention further comprises at least one promoter, enhancer, intron and/or polyA-sequence. Preferred promoters or enhancers posses tissue specificity, in particular neuronal specificity and more particular a specificity for growing neurons. Examples of such promoters and/or enhancers are the neuron specific enolase promoter (Erickson, R.P. and Bernard, O. (2002) J. Neuro Science Res 68:738-44),

the peripherin promoter (Weinstein, D.E. et al. (1999) Brain Res. Dev. Brain Res. 116:29-39), the synapsin promoter (Flood, D.G. et al. (1999) Am. J. Pathol. 155:663-72) and the Thy 1 promoter (Kahle, P. J. et al. (2001) Am. J. Pathol. 159:2215-25).

In some instances it might be desirable to interfere with, for example, the transcription or translation of the nucleic acids of the present invention and, therefore, the present invention is also directed at a nucleic acid, which is complementary to the nucleic acid of the present invention and, thus, is capable of inhibiting, for example, transcription or translation. A preferred embodiment of such a complementary nucleic acid is a so called anti-sense oligonucleotide (R. Q. Zheng and D. M. Kemeny (1995) Clin. Exp. Immunol. 100:380-2, W. Nellen and C. Lichtenstein (1993) Trends. Biochem. Sci. 18:419-423 and C. A. Stein (1992) Leukemia 6:967-74), ribozymes (M. Amarzguioui and H. Prydz (1998) Cell. Mol. Life Sci. 54:1175-1202, N. K. Vaish et al (1998) Nucleic Acids Res. 96:5237-5242, Persidis (1997) Nat. Biotechnol. 15:921-922 and L. A. Couture and D. T. Stinchcomb (1996) Trends Genet. 12:510-515) and/or so called small interfering RNA-molecules (siRNAs) (S. M. Elbashir et al. (2001) Nature 411:494-498). Anti-sense oligonucleotides are able to decrease the stability of the above described nucleic acids and/or can inhibit the translation. Similarly the use of siRNA-oligonucleotides can also lead to a reduction in the amount of the translated polypeptides. Anti-sense oligonucleotides have in a preferred embodiment a length of at least 20, preferable of at least about 30, more preferably of at least about 40 and most preferably a length of at least about 50 nucleic acids.

Oligonucleotides are generally rapidly degraded by endo- or exonucleases, which are present in the cell, in particular by DNases und RNases and, therefore, it is advantageous to modify the nucleic acids which are used, for example, in anti-sense strategies, as ribozymes or siRNAs to stabilize them against degradation and thereby prolong the time over which an effective amount of the nucleic acid is maintained within the cell (L. Beigelmann et al. (1995) Nucleic acids Res. 23:3989-94, WO 95/11910, WO 98/37340 and WO 97/29116). Typically such stabilization can be obtained by the introduction of one or more internucleotide phosphate groups and/or by the introduction of one or more non-phosphor-internucleotides.

Suitable modified internucleotides are summarized in, for example, Uhlmann and Peimann (1990) Can. Rev. 90:544. Modified internucleotide phosphate residues and/or non-

phosphate bridges which can be used in a nucleic acid of the invention comprise, for example, methylphosphonate, phosphorthioate, phosphoramidate, phosphordithionate, phosphate ester, non-phosphor internucleotide analogues, which can be used in nucleic acids of the invention include, for example, siloxane bridges, carbonate bridges, carboxymethylester, acetamid bridges and/or thioether bridges.

A further aspect of the present invention is directed at a vector comprising a protein according to the present invention and/or a nucleic acid according to the present invention. A vector within the meaning of the present invention is a protein or a nucleic acid or a mixture thereof which is capable of being introduced or of introducing the proteins and/or nucleic acid comprised into a cell. It is preferred that the proteins encoded by the introduced nucleic acid are expressed within the cell upon introduction of the vector.

In a preferred embodiment the vector of the present invention comprises plasmids, phagemids, phages, cosmids, artificial mammalian chromosomes, knock-out or knock-in constructs, viruses, in particular adenovirus, vaccinia virus, lentivirus (Chang, L.J. and Gay, E.E. (20001) Curr. Gene Therap. 1:237-251), Herpes simplex virus (HSV-1, Carlezon, W.A. et al. (2000) Crit. Rev. Neurobiol.), baculovirus, retrovirus, adeno-associated-virus (AAV, Carter, P.J. and Samulski, R.J. (2000) J. Mol. Med. 6:17-27), rhinovirus, human immune deficiency virus (HIV), filovirus and engineered versions thereof (see, for example, Cobinger G. P. et al (2001) Nat. Biotechnol. 19:225-30), virosomes, "naked" DNA liposomes, and nucleic acid coated particles, in particular gold spheres. Particularly preferred are viral vectors like adenoviral vectors or retroviral vectors (Lindemann et al. (1997) Mol. Med. 3:466-76 and Springer et al. (1998) Mol. Cell. 2:549-58). Liposomes are usually small unilamellar or multilamellar vesicles made of neutral cationic and/or anionic lipids, for example, by ultrasound treatment of liposomal suspensions. The DNA can, for example, be ionically bound to the surface of the liposomes or internally enclosed in the liposome. Suitable lipid mixtures are known in the art and comprise, for example, cholesterol, phospholipide like, for example, phosphatidylcholin (PC), phosphatidylserin (PS) and the like, DOTMA (1, 2-Dioleyloxpropyl-3-trimethylammoniumbromid) and DPOE (Dioleoylphosphatidylethanolamin) which both have been used on a variety of cell lines.

Nucleic acid coated particles are another means for the introduction of nucleic acids into cells using so called "gene guns", which allow the mechanical introduction of particles into

the cells. Preferably the particles itself are inert, and therefore, are in a preferred embodiment made out of gold spheres.

In a further aspect the present invention is directed at an isolated cell comprising a protein of the present invention, a nucleic acid of the present invention and/or a vector of the present invention. Cells of the present invention can be prokaryotic or eukaryotic cells and in a preferred embodiment the cells of the present invention are stem cells, in particular non-human embryonic stem cells, embryonic stem cell lines, foetal stem cells, adult stem cells, neuronal precursor cells or neuronal cells in particular axons (Hsich, G. et al. (2002) Hum. Gene Therap., 13:579-604 and Martinez-Serrano, A. et al. (2001) Curr. Gene Therap. 1:279-299). The cells preferably comprise the nucleic acids extrachromosomally or interchromosomally.

A further aspect of the present invention is a transgenic non-human animal generated from a cell or cells of the present invention. The animal can be a mosaic animal, which means that only part of the cells making up the body comprise cells of the present invention or the animal can be a transgenic animal which means that all cells of the animal are derived from a cell of the present invention. Mosaic or transgenic animals can be either homo- or heterozygous with respect to the nucleic acid of the present invention contained within the cell of the present invention. In a preferred embodiment the transgenic animals are either homo- or heterozygous knock-out or knock-in animals with respect to the genes which code for the proteins of the present invention.

In a further aspect the present invention is directed at an antibody directed against a protein of the present invention. The term "antibody" comprises monoclonal and polyclonal antibodies and binding fragments thereof, in particular Fc-fragments as well as so called "single-chain-antibodies" (Bird R. E. et al (1988) Science 242:423-6) and diabodies (Holliger P. et al (1993) Proc. Natl. Acad. Sci. U.S.A. 90:6444-8).

In a further aspect the present invention is directed at a method of producing a protein of the present invention or a nucleic acid of the present invention and comprises the steps of: a) cultivating a cell of the present invention and b) isolating the protein and/or the nucleic acid. If the method is used primarily to isolate nucleic acids then in an preferred embodiment the cells, which are used are prokaryotic cells, in particular *E. coli.* cells If the

method is used primarily for the isolation of proteins of the invention than the cells can be either of prokaryotic or eukaryotic origin. Someone of skill in the art is aware of a variety of different cell types suitable for the production of proteins like, for example, *E. coli*, Sf9, Hi5, *P. pastoris*, COS and HeLa. Eukaryotic cells are preferably chosen, if it is desired that the proteins produced by the cells exhibit an essentially natural pattern of glycosylation and prokaryotic cells are chosen, if, for example, glycosylation or other modifications, which are normally introduced into proteins only in eukaryotic cells, are not desired or not needed.

In a further aspect the present invention is directed at a method of isolating compounds interacting with a protein of the present invention comprising the steps of: a) contacting one or more of the proteins of the present invention, preferably one, with at least one potentially interacting compound, and b) measuring binding of said compound to said protein. This method is suitable for the determination of compounds that can interact with the proteins of the present invention and to identify, for example, inhibitors, activators, competitors or modulators of proteins of the present invention, in particular inhibitors, activators, competitors or modulators of the enzymatic activity of the proteins of the present invention.

The potentially binding substance, whose binding to the protein of the present invention is to be measured, can be any chemical substance or any mixture thereof. For example, it can be a substance of a peptide library, a combinatory library, a cell extract, in particular a plant cell extract, a "small molecular drug", a protein and/or a protein fragment.

The term "contacting" in the present invention means any interaction between the potentially binding substance(s) with the proteins of the invention, whereby any of the two components can be independently of each other in a liquid phase, for example in solution, or in suspension or can be bound to a solid phase, for example, in the form of an essentially planar surface or in the form of particles, pearls or the like. In a preferred embodiment a multitude of different potentially binding substances are immobilized on a solid surface like, for example, on a compound library chip and the protein of the present invention is subsequently contacted with such a chip.

The proteins of the present invention employed in a method of the present invention can be full length proteins or a fragments with N/C-terminal and/or internal deletions. Preferably the fragments are either N-terminal fragments comprising the enzymatic region of the protein or C-terminal fragments comprising the cytoplasmic region, depending on whether potentially interacting compounds are sought that specifically interact with the N- or C-terminal fragment

Measuring of binding of the compound to the protein can be carried out either by measuring a marker that can be attached either to the protein or to the potentially interacting compound. Suitable markers are known to someone of skill in the art and comprise, for example, fluorescence or radioactive markers. The binding of the two components can, however, also be measured by the change of an electrochemical parameter of the binding compound or of the protein, e.g. a change of the redox properties of either the protein or the binding compound, upon binding. Suitable methods of detecting such changes comprise, for example, potentiometric methods. Further methods for detecting and/or measuring the binding of the two components to each other are known in the art and can without limitation also be used to measure the binding of the potential interacting compound to the protein or protein fragments of the present invention. The effect of the binding of the compound or the activity of the protein can also be measured indirectly, for example, by assaying the phosphatase activity of the protein after binding.

As a further step after measuring the binding of a potentially interacting compound and after having measured at least two different potentially interacting compounds at least one compound can be selected, for example, on grounds of the measured binding activity or on grounds of the detected increase or decrease of protein activity, in particular lipid phosphate phosphatase activity upon binding. The phosphatase activity can be measured, for example, as described in example 11.

The thus selected binding compound is than in a preferred embodiment modified in a further step. Modification can be effected by a variety of methods known in the art, which include without limitation the introduction of novel side chains or the exchange of functional groups like, for example, introduction of halogens, in particular F, Cl or Br, the introduction of lower alkyl groups, preferably having one to five carbon atoms like, for example, methyl, ethyl, n-propyl, isopropyl, n-butyl, isobutyl, tert-butyl, n-pentyl or iso-

pentyl groups, lower alkenyl groups, preferably having two to five carbon atoms, lower alkinyl groups, preferably having two to five carbon atoms or through the introduction of, for example, a group selected from the group consisting of NH_2, NO_2, OH, SH, NH, CN, aryl, heteroaryl, COH or COOH group.

The thus modified binding substances are than individually tested with the method of the present invention, i.e. they are contacted with the protein and subsequently binding of the modified compounds to the protein is measured. In this step both the binding per se can be measured and/or the effect of the function of the protein like, e.g. the enzymatic activity of the protein can be measured. If needed the steps of selecting the binding compound, modifying the binding compound, contacting the binding compound with a protein of the invention and measuring the binding of the modified compounds to the protein can be repeated a third or any given number of times as required. The above described method is also termed "directed evolution" since it involves a multitude of steps including modification and selection, whereby binding compounds are selected in an "evolutionary" process optimizing its capabilities with respect to a particular property, e.g. its binding activity, its ability to activate, inhibit or modulate the activity, in particular the phosphatase activity of the proteins of the present invention.

A further aspect of the present invention is a method of isolating compounds functionally interacting with the activity of the proteins of the present invention comprising the steps of: a) contacting a neuronal cell that comprises a wt nucleic acid coding for a protein selected from the group consisting of SEQ ID NOs: 1 to 12, a splice variant thereof, or a fragment thereof with a potential functional interactor, b) contacting the cell with a bioactive lipid phosphate, and c) measuring neurite movement or phosphatase activity.

The term "contacting" has to be understood as previously defined and comprises any possibility of interaction between the potential functional interactor and a neuronal cell. Contacting also comprises the introduction of the potential functional interactor into the neuronal cell which can be effected by a variety of methods including, for example, electroporation, which allows influx of a potential functional interactor contained in the medium surrounding the neuronal cell into the neuronal cell. A neuronal cell that comprises a wt nucleic acid coding for a PRG protein (as indicated in SEQ ID NOs: 1 to 12) can be any neuronal cell capable of neurite movement. The cell may or may not express the wild-type

nucleic acid depending on, for example, the developmental stage of the neuronal cell. For example entorhinal cortex cells of embryonic day 16 (E16), which exhibit neurite movement, do not express PRG-1 while entorhinal cortex cells of postnatal day 0 (P0) do express PRG-1. The choice of either a cell that already expresses or does not express the wild-type nucleic acids will depend on the functional interaction of the potential functional interactor that is sought. If, for example, a functional interactor is sought, that activates transcription within the cell normally not expressing PRG-1 than, for example, an E16 cell could be chosen. If functional interactors are sought that primarily interact on the protein level, i.e. that activate or suppress phosphatase activity of already expressed PRG-1 than neuronal cells expressing PRG-1 would be chosen like, for example, P0 cells.

Bioactive lipid phosphates are lipid phosphates which inhibit neurite movement of neuronal cells, which do not express PRG-1, like for example, E16 cells. Examples of such bioactive lipid phosphates comprise PA, LPA and S-1-P. Whether a lipid phosphate, which can be used in the method of the present invention is bioactive can be determined by, for example, the experiment described in Example 9.

Methods for measuring neurite movements are well-known in the art and are described, for example, in Savaskan et al. (1999) European J. Neurosci. 11:319-326. One way of measuring neurite movement is scoring of the cells after contacting with a bioactive lipid phosphate. It is possible to categorize the cells into at least three different categories, i.e. round cells, cells with short processes and cells with long processes. It is also possible to quantify the effect by measuring the length of the neurite processes. The effect of the potential functional interactor can be determined by comparing the neurite movement of the neuronal cell, the categories the cells are in or the length of the neurite processes after contacting the cell with a bioactive lipid phosphate with or without the functional interactor. Other ways to assess the effect of potential functional interactors are the determination of the expression level of the PRG genes and/or proteins or the enzymatic activity of the proteins.

In a further embodiment the method includes the additional steps of: a) contacting a neuronal cell that comprises a mutant nucleic acid coding for a mutant of the proteins selected from the group consisting of SEQ ID NOs: 1 to 12, a splice variant thereof, or a fragment thereof or that contains a knock-out of the wt nucleic acid coding for one of said proteins with a potential functional interactor, b) contacting said cell with a bioactive lipid phos-

phate, and c) measuring neurite movement. The above described neuronal cell is preferably incapable of expressing a functional PRG protein and, thus, can not be stimulated by any functional interactor to activate PRG genes or PRG protein function. Therefore, any potential functional interactor, which shows an effect on the neurite movement of neuronal cells comprising wild-type PRG genes but shows no effect in the neuronal cell comprising mutants or knock-out PGR genes have thereby been shown to functional interact with the PRG genes. Once such an interactor has been identified the mode of functional interaction can be further analyzed and to that end the amount of PRG mRNA and/or protein expressed or the activity of the PRG protein can be determined by a variety of different techniques, which are either known in the art or described herein.

In a preferred embodiment the method of the invention comprises the further steps of: a) modifying the functional interactor to generate a variety of modified functional interactors, b) contacting a neuronal cell comprising a wild-type nucleic acid coding for a protein selected from the group consisting of SEQ ID NOs: 1 to 12, a splice variant thereof, or a fragment thereof and if needed a cell that comprises a mutant nucleic acid coding for a mutant of the protein selected from the group consisting of SEQ ID NOs: 1 to 12, a splice variant thereof, or a fragment thereof with the modified functional interactors, c) contacting said cell or cells with a bioactive lipid phosphate, d) measuring the neurite movement, and e) if needed repeating steps a) to d) for one or more times. The modification of the functional interactor can be any of the modifications outlined above with respect to the modification of an interacting compound and the modification and selection steps can be repeated one or several times until a functional interactor has been selected that shows the desired functional interaction, e.g. repression or activation of the activity in particular of the enzymatic activity of PRG proteins.

In a further embodiment of the method of the present invention the interacting compound identified as outlined above or the functional interactor identified as outlined above, which may or may not have gone through additional rounds of modification and selection, is admixed with suitable auxiliary substances and/or additives. Such substances comprise pharmacological acceptable substances, which increase the stability, solubility, biocompatibility, or biological half-life of the interacting compound or the functional interactor or comprise substances or materials, which have to be included for certain routs of application like, for example, intravenous solution, sprays, Band-Aids or pills.

Since expression of PRG-1 can prevent LPA induced neurite retraction and/or expression of rat PRG-3 induces neurite extension these proteins have another utility in the treatment of neuronal injuries and diseases. Accordingly a further aspect of the present invention is a pharmaceutical composition for the treatment of neuronal injuries or diseases comprising a protein of the invention, a nucleic acid of the invention, a vector of the invention, a cell of the invention, an antibody of the invention, a binding component isolated by a method of the invention and/or a functional interactor isolated by a method of the invention and if needed suitable auxiliary substances and/or additives.

Accordingly, a further aspect of the present invention is the use of a pharmaceutical composition of the invention for the production of a medicament for the treatment of neuronal diseases or injuries. Neuronal diseases which can be treated with the pharmaceutical composition comprise spinal cord lesion, Alzheimer disease and stroke. Typical neuronal injuries comprise traumata of any sort in particular head traumata resulting in the damage of neurons and in particular the severing of neuronal connections.

As stated above it has also been found that PRG proteins are differentially expressed in certain tissues and that they have been found to be differentially expressed in certain diseases, however, differential expression is also associated with certain disease states. Thus, PRG proteins present attractive targets for diagnosis and treatment of a variety of diseases. Therefore, another aspect of the present invention is the use of the proteins or nucleic acids of the present invention as diagnostic marker for the diagnosis of a disease or disease state, whereby the presence, the absence, or the amount of PRG proteins is evaluated by, for example, immunological methods, RT-PCR, Northern blot. For the immunological detection and/or quantification methods the antibodies of the present invention can be used.

As PRG is differentially regulated in neuronal diseases PRG proteins or nucleic acids are in a preferred embodiment used as diagnostic marker for the diagnosis of neuronal diseases.

Furthermore PRG proteins are overexpressed in tumors. PRG-1, for example, is overexpressed in a variety of tumor cells, e.g. astroglioma WHO Grad III-IV, neuroblastoma, kidney cell carcinoma, myoblastoma and ovarial cell carcinoma, and in particular it has

also been found to be overexpressed in migrating, i.e. metastasizing cancer cells which have lost the anchorage dependence for growth. Therefore, PRG proteins also present attractive targets for diagnoses and treatment of tumors, in particular metastasizing tumors. Consequently, a further aspect of the present invention is the use of PRG proteins and nucleic acids of the present invention as a tumor markers and, preferably, as metastatic markers. Because of the above property PRG proteins are also therapeutic targets for the development of drugs, which modulate, preferably inhibit the function of PRG proteins. Such drugs can be identified with above-described methods for identifying interacting or functional interacting compounds.

In a preferred embodiment, PRG proteins of the present invention are used for diagnosis of cancers selected from the group of cancers consisting of neuroblastoma, astroglioma, ovarial cell carcinoma, prostatic cell carcinoma and breast cell carcinoma.

In addition, PRG proteins, in particular PRG-1, have been found to be overexpressed in differentiating sperm cells and, thus, a further embodiment of the present invention is the use of the PRG proteins or nucleic acids as diagnostic targets for the diagnosis of infertility, in which a lack of PRG proteins would indicate either a low amount of differentiating sperm cells or the malfunction of the sperm cells. The amount of expression of PRG proteins or nucleic acids can be detected by, for example, *in situ* immunofluorescence, *in situ* Northern blots. The skilled persons knows a variety of additional methods that are suitable to determine the amount and distribution of PRG proteins and RNA within a cell ansd/or tissue.

The following figures and examples merely serve to illustrate the invention and should not be construed to restrict the scope of the invention to the particular embodiments of the invention described in the examples. All references cited in the text and the disclosure of the priority applications EP 02 020 679.3 and EP 03 002 993.8 are hereby incorporated in their entirety by reference.

Figures

Fig. 1 Panel A depicts the human PRG-1 amino acid sequence (SEQ ID NO. 1). The first 300 amino acids are highly conserved among LPP family members. The

other 400 amino acids (gray boxed sequence) of PRG-1 show no homologies to known sequences. The catalytic histidine (His-252) is marked with an asterisk. Panel B depicts rPRG-3 (SEQ ID NO. 11). Start and stop codons are marked with a dark box. Putative transmembrane domains are underlined in grey, the C-terminal tail is indicated light grey. The probes, which were used for *in situ* hybridization are marked with a black line.

Fig. 2 Panel A depicts the hydrophobicity profile of human PRG-1 protein predicted by the Kyte and Doolittle algorithms. The gray shaded area of PRG-1 is predicted as hydrophilic and located in the cytosol. Panel B depicts the hydrophobicity profile of rat PRG-3-protein. The numbers at the bottom of the profiles refer to amino acid residues from the amino terminus. Panel C depicts the *in silico* determined phylogenetic tree of different PRG-proteins and LPP-1.

Fig. 3 Northern blot analysis of PRG-1 mRNA expression

Fig. 4 Expression pattern of PRG-1 mRNA in the developing and lesioned rat brain detected by *in situ* Northern blot. Panel A shows the Toluidene blue staining of a brain section on embryonic day 16 (E16). Panel B shows the *in situ* hybridization signal with a probe specific for PRG-1 mRNA of the same section as shown in panel A. Panel C shows a Toluidene blue staining of a brain section on embryonic day 19 and panel D shows the *in situ* hybridization with a probe specific for PRG-1 mRNA of the same section as shown in panel C. Panels E through K show *in situ* Northern blot analysis of brain sections at days 0, 5, 10, 15, 30 after birth, in an adult and one day after lesion, respectively. The scale bar in E19 equals 850 µm. The scale bar in P30 equals 740 µm and also applies to P0-P15. The scale bar in 1dal equals 500 µm and also applies to adult. "LV" means lateral ventricle, "LP" means lateral posterior thalamic nucleus, "LD" means laterodorsal thalamic nucleus, "bcp" means basal telencephalic plate, posterior part, "CA1" means cornu ammonis, "DG" means dentate gyrus, "RSG" means retrosplenial granular cortex, "dal" means days after lesion.

Fig. 5 Quantification of the *in situ* hybridization signals in different regions of the brain after lesion. "gcl" means granule cell layer, "CA3" means cornu ammonis 3, "CA1" means cornu ammonis and "dal" means days after lesion.

Fig. 6 Overexpression of a PRG-1-eGFP fusion protein in COS-7 cells. Panel A shows the fluorescence of the green fluorescent protein, panel B shows the fluorescence of a fluorecently labeled anti-PRG-1 peptide antibody and panel C shows the co-localization of the fluorescence of the PRG-1-eGFP and the anti-PRG-1 antibody. In each picture the processes of the COS-7 cells are marked with a white arrow. The scale bar depicts a length of 10 µm. Panel D shows the result of a Western blot using an antiserum raised against a C-terminal peptide of PRG-1.

Fig. 7 Immunocytochemical analysis of PRG-1 in the adult rat hippocampus prior and after lesion. Pyramidal neurons are labeled in the CA1 and CA3 region. Polymorphic cells are stained in the hilus. The outermoelcular layer is marked with black errors. "Gcl" means granule cell layer "Oml" means outer molecular layer and "hi" means hilus. The scale bar in panel A and B equals 580 µm. Panel C shows immunoblots from total protein extracts of adult control and deafferentiated hippocampus five days after lesion.

Fig. 8 Panel A shows a higher magnification of the boxed area of panel B of Fig. 7. Immuno-stained axons are marked with black arrows and the terminal branches with white arrows. Panel B shows an electron micrograph of a PRG-1 immunopositive axon. The immunopositive axon is delineated by black arrows, while its terminal branch is delineated by gray arrows. "oml" means outer molecular layer and "ax" means axon and "s" means spine. The scale bar in panel A equals 20 µm and the scale bar in panel B equals 0.4 µm.

Fig. 9 Panel A-C show the result of an RT-PCR analysis of RNA from tissues from E16 and P0 explants. The amplification was carried out with primers specific for PRG-1 (panel A), EDG 2, 4 or 7 (panel B) and β-actin (panel C). Panel D and E depict explants from rat entorhinal cortex at embryonic day 16 and panel F and G depict rat entorhinal cortex at postnatal day 0 (bottom row of panels). Outgrowing axons are marked with white arrows and the panels D and F show neu-

rite retraction in the presence of vehicle (0,9% NaCl) while panels E and G show neurite retraction upon the addition of 100 nmol/l LPA. The scale bar in panel G equals 20 µm.

Fig. 10 Panel A shows the neurite outgrowth length in control cultures (left bar) and LPA treated cultures, (right bar) in E16 and postnatal explants (P0) in µm. Panel B shows the dose-response of LPA on P0 and E16 explants.

Fig. 11 Depicts cell rounding and neurite retraction in response to LPA in N1E-115 cells. The cells depicted in the first three top panels were transfected with a plasmid containing only eGFP and were not treated with LPA but with vehicle only. The cells in the second row were transfected with a plasmid containing only eGFP but were treated with 10 µmol/l LPA, the cells of the third row were transfected with a plasmid coding for a PRG-1-eGFP fusion protein and were treated with 10 µmol/l LPA while the cells depicted in the bottom row of panels were transfected with a mutant PRG-1-eGFP fusion protein, which carried a His-Lys exchange in the catalytic histidine of PRG-1 (PRG-$1^{His/Lys}$) and were also treated with 10 µmol/l LPA. The panels on the left show transfected cells, panels in the middle show nuclear staining (Hoechst staining) and panels on the right show merged images with f-actin staining.

Fig. 12 Panel A shows the quantification of the results shown in Fig. 11 and of a similar experiment performed with wild type N1E-115 cells (wt). Panel B shows the results of RT-PCR using LPA receptor specific primers to assess LPA receptor expression in wild type N1E-115 cells (wt) or PRG-1 transfected N1E cells (PRG-1). Panel C shows the results of RT-PCR using β-actin specific primers to assess β-actin expression in wt N1E-115 cells and in PRG-1 transfected cells. Panel D shows a dose response of LPA treatment on neurite length of PRG-1 overexpression cells. Panel E shows cell viability of N1E-115 cells 48-72 h after transfection. Panel F shows the phosphatase activity of intact cells overexpressing eGFP, PRG-1-eGFP, and PRG-$1^{His/Lys}$.

Fig. 13 Schematic diagram of the proposed axon growth mechanism in a lipid phosphate lipid rich environment. "R" means receptor mediating a retraction signal.

Fig. 14 Depicts the proposed structure of the human PRG-1 wherein those parts presumed to be arranged on the extracellular surface inserted in the plasma membrane and protruding into the cytoplasm are shown.

Fig. 15 Expression pattern of PRG-3 mRNA in the developing rat brain detected by *in situ* Northern blot. Panels A-C depict the in *in situ* staining of rat brain sections at various developmental stages in which E18 and E20 depict stains from embryonic days 18 and 20, and P0, P5, P10, P15 stains post partum at days 0, 5, 10, and 15. The scale bar in A equals 1.8 mm and in panel B 400 µm. Panel D depicts the Northern blot analysis of RNA derived from different tissues of the adult rat.

Fig. 16 Depicts the cellular localization of PRG-3-eGFP fusion proteins. PRG-3 is visible predominantly in the plasma membrane and in neurite extensions. The upper row depicts cells transfected with the peGFP-N1 reporter vector alone and the second and third row cells transfected with a pPRG-3-eGFP fusion construct. The scale bar in the second row represents 2 µm and 5 µm in the third row.

Examples

1. Isolation of PRG-1

Animals and surgery

All animals were housed under standard laboratory conditions, and the surgical procedures were performed in agreement with the German law (in congruence with 86/609/EEC) for the use of laboratory animals. All efforts were made to minimize the number of animals used, and all surgical procedures were performed under sufficient anesthesia to minimize animal suffering. The experimental procedures are described in detail in Bräuer et al (2001) FASEB J. 15:2689-2701.

Substraction cDNA library and differential screening

The SMART cDNA technology from Clontech was used to generate high yields of full-length, double-stranded cDNA from adult, control and lesioned hippocampus rat RNA. To

develop the substraction library, the Clontech PCR-Select cDNA substraction Kit (Heidelberg, Germany) was used. Each clone was dotted in duplicates on Hybond N filters (Amersham, Germany) and screened with randomly radioactively labeled cDNA (Prime-A-Gene, Promega, Germany) from adult non-lesioned and lesioned hippocampus.

2. Analysis of the sequence of PRG-1

Similar to other members of LPP-family a hydrophobicity analysis of PRG-1 predicts 6 N-terminal membrane-spanning regions with a highly conserved phosphatase domain. The analysis was done using the DNAsis for Windows Version 2.6; Hitachi Software Engineering Co. Hydrophobicity Analysis Submenue using the Kyte & Doolittle algorithm with all settings set to default values. However, unlike the other members of this family the second type of the protein consists of a long hydrophilic domain of around 400 amino acids (Fig. 2). According to the structural models of LPP orientation in the membrane, this C-terminal extension is positioned on the cytoplasmatic site and might thus play a role as a regulatory or signal transduction domain. Beside the homology of the N-terminal part of the PRG-1 to other members of the LPP-family such as LPP-1 and the Drosophila cell migration modulator Wunen, GenBank searches revealed only one other related gene (genomic DNA sequence: GenBank acc. # NP_011255.11) for which we cloned the complete cDNA sequence and named it PRG-2. This gene shares the same C-terminal extension with partial sequence homology. Thus, these genes represent a novel distinct subclass of the LPP-1 family. Amino acid residues which have been shown to be essential for ecto-enzyme activity in the LPP-1 class of proteins are conserved in PRG-1 N-terminal sequences (Fig. 1). Database analysis of the C-terminal domains did not detect any significant similarities to any other protein or any other matches with known conserved domains (using ProDom and Swiss-Prot databases). A GenBank search for orthologous proteins showed that both genes are highly conserved in mammals (human/mouse > 93%), and partial EST sequences indicate orthologous proteins in Xenopus and Zebrafish, whereas no significant homology for the C-terminal part could be found in the Drosophila or other invertebrate genome.

3. Northern blot analysis of PRG-1 expression

20 µg of total RNA from six adult control and six 1 dal animals were loaded on a 1% agarose gel containing formaldehyde, transferred to Hybond™ – Ns (Amersham Life Science, UK) and crosslinked by ultraviolet irradiation. As a probe for PRG-1, the full length cDNA

clone as well as the C-terminal coding region was used. As probe for β-actin (as control for mRNA integrity and amounts of mRNA loaded), a cDNA fragment amplified by RT-PCR was used. Primer for the amplification of the control gene β-actin were: β-actin 5' (5'–CAC CAC AGC TGA GAG GGA AAT CGT GCG TGA – 3', SEQ ID No. 25) spanning bases 2395 – 2424, and β-actin 3'-primer (5'–ATT TGC GGT GCA GCA TGG AGG GGC CGG ACT–3', SEQ ID no. 26) complementary to bases 3095 – 3124, with an amplificate length of 520 bp for rat β-actin cDNA (GenBank accession no. J00691). PCR was performed in 25 µl final volume containing 1 mmol/l dNTPs (Pharmacia Biotech, Germany), 2.5 units Taq Polymerase (Perkin Elmer, USA) 2.5 µl 10 x buffer including 2.5 mol/l $MgCl_2$ (Perkin Elmer, USA), 10 µmol/l each primer and 1 µl cDNA using a Thermo-Cycler PTC-100 (MJ Research, Inc., USA). The cycle program was: 95°C, 2 min; 35 x [94°C, 30 s; 70°C, 30 s 72°C, 2 min] and 10 min, 72°C. Both probes were labeled with the Prime-a-Gene Labelling System (Promega, USA) and [^{32}P] dCTP (DuPont NEN, USA). Hybridization was performed in 10 ml hybridization solution (250 mmol/l sodium-phosphate, pH 7.2, 7% SDS, 0.5 mmol/l EDTA, 1% BSA) at 60°C for 12 h. The membrane was washed in 2 x SSC at RT, 0.2 x SSC at RT, and 0.2 x SSC at 40°C for 30 min each. Membranes were exposed to Kodak X-OMAT AR X-ray films at –80°C for 12 h, using an intensifying screen. Northern blot analysis revealed one distinct band which migrated around 5,5 kb. Expression of this mRNA was CNS-specific with the exception of a weak expression in testies (see Fig. 3). Thus, PRG-1 is a novel vertebrate specific protein selectively located in the brain with putative phosphatase function.

4. *In situ* hybridization analysis of PRG-1 expression

For hybridization, an antisense oligonucleotide (5'-GCA GAG GTC TGA ATT CTA GTG TCT ATC GTT ATA GTT CCT TAA CAG TGT GGG-3', SEQ ID No. 27) complementary to bases 425 – 475 of a rat EST cDNA clone (GenBank acc. AW 526088.1) was used. The oligonucleotide was synthesized by Metabion (Munich, Germany). The specificity was confirmed by a BLAST GenBank search to rule out cross-hybridization to other genes. The protocol was used as described by Bräuer et al (2002) *supra*.

The *in situ* hybridization analysis highlighted the tight regulation of PRG-1 transcription in the developing hippocampus. At embryonic day 16 (E16), no PRG-1 transcripts could be detected in the brain (Fig. 4, panel B). An expression signal first appears at day 19 (E19) in the subventricular zone and specifically in the hippocampal anlage, whereas other cortical

regions did not show PRG-1 expression (Fig. 4, panel D). From postnatal stages on, PRG-1 mRNA is present in the hippocampus and in the entorhinal cortex throughout adult stages (see Fig. 4, panels E-J). In the dentate gyrus, a region bearing postnatally developing granule cells, weak PRG-1 mRNA expression is found in the infrapyramidal blade at P0, whereas the later developing suprapyramidal blade first showed expression signals at P5. This expression pattern remains unchanged during maturation, however, a reduced expression is apparent in the adult brain.

5. PRG-1 mRNA expression after entorhinal cortex lesion

The treatment of the animals, the surgery the construction of the subtraction cDNA library and the screening were carried out as described in example 1. The *in situ* hybridization was carried out as described in example 4. PRG-1 is upregulated one day after lesion (dal) and peaks at 5 dal in the ipsilateral hippocampus (gcl = 37%, hilus 300%, CA1 = 100%, CA3 = 60%). The contralateral hippocampus (maximum by 1 dal, gcl = 16%, hilus = 200%, CA1 = 59%, CA3 = 46%), as well as the ipsilateral cortex, shows a strong upregulation of PRG-1 mRNA (maximum by 1 dal 83%) (see Fig. 5).

6. Transfection of a PRG-1-eGFP construct

Antibody generation and immunohistochemistry

To design a peptide antibody against PRG-1, a sequence in the hydrophilic C-terminal region was used. The peptide (NH_2-CVGVNGDHHVPGNQ-COOH, SEQ ID No. 28), representing amino acids 490 – 507 of the PRG-1 rat sequence (SEQ ID No. 9), was synthesized by BioGenes (Berlin, Germany). The amino-terminal cysteinyl residue, which is not part of the PRG-1 sequence, was included for conjugation of the peptide to a carrier protein. The peptide was conjugated through the cysteinyl sulfhydryl to maleimide activation (keyhole limpet hemocyanin). Rabbits were immunized by BioGenes. The specificity of the peptide antibody was further tested on Western blot and on brain sections by blocking via peptide incubation prior to adding the antiserum. The protocol for the immunohistochemistry is described in detail by Bräuer et al (2001) Neuroscience 102:515-526.

Western Blot analysis

For Western Blot analysis, rat adult and 5 dal hippocampus extracts were separated on a 12% SDS/PAGE and electroblotted to nitrocellulose membranes (Millipore, Germany). All incubation was done overnight at 4°C in PBST. The PRG-1 antiserum was used at a

1:2000 dilution. Secondary anti-rabbit antibody coupled with horseradish peroxidase was used at a 1:5000 dilution, and visualized by incubation in ECL detection reagents (Amersham Pharmacia, Germany). The protocol for the immunocytochemistry is essentially the same as described in detail in Bräuer et al. (2001) supra].

The immunoblot in Fig. 6D showed a single band obtained by incubation with the anti-PRG-1 antiserum. The absence of specific signal in the preimmune serum prior to immunization is noteworthy. Immunoblots from total protein extracts of adult control and deafferentiated hippocampus shown in Fig. 7C demonstrated an increase five days after lesion (5dal). Data represents three separate experiments in each group. Statistical difference is marked with an asterisk (mean ± S.D.), * $P < 0.05$; Mann-Whitney-*U*-test.

Subcellular localization

PRG-1 tagged with the eGFP reporter gene was used to identify the subcellular localization. Golgi apparatus was visualized with the cell tracker BODYPY ceramide (Molecular Probes, Netherlands). The staining protocol was obtained from molecular Probes.

The transfection studies using a PRG-1 construct tagged with a eGFP reporter gene revealed that PRG-1 protein was processed in COS-7 cells through the Golgi apparatus (data not shown) to its final localization in the plasma membrane of small processes (Fig. 6, panel A). To localize the PRG-1 proteins *in vivo* an antiserum against a peptide from the cytoplasmic C-terminus of PRG-1 was raised. This antiserum specifically stained transfected COS-7 cells, which expressed PRG-1-eGFP fusion proteins (Fig. 6, panel A-C) and detected a specific band in Western blot analysis (Fig. 6, panel B). Both the immunostaining and Western blot signal could be blocked by specific peptide incubation prior to the addition of antiserum (data not shown). The fluorescence of the labeled entire-PRG-1 peptide antibody and the fluorescence of the eGFP part of the fusion protein colocalized in COS-7 cells and in the processes (see white arrows in panels A-C of Fig. 6).

7. Expression analysis by RT-PCR

Tissue from the retraction assays, E16 and P0 explants and N1E-115 cells were used for mRNA isolation and as templates for RT-PCR. cDNA from testis was used as a positive control. The MidiMACS mRNA Isolation Kit (Miltenyi Biotec, Germany) was used to

isolate mRNA from the explants or cells. Reverse transcription was performed as described by Bräuer et al. (2000) Hippocampus 10:632-644. PCR was performed with the following primers: PRG-1-5'-primer (5'-CTA GGC TTG TAG CTG TGG GGA ATT TC-3', SEQ ID No. 29), spanning bases 896 bp –921 bp, and PRG-1-3'primer (5'-TCA ATC CTT ATA AGC CCG TGT G-3', SEQ ID No. 30) complementary to bases 2202 bp – 2225 bp with an amplification length of 1329 bp of the PRG-1 cDNA (SEQ ID No. 21). For amplification of the EDG receptor cDNA, the primer EDG-2-5' primer (5'-GAA CTT TGC GAG TGA GCT GG-3', SEQ ID No. 31), spanning bases 836 bp –855 bp, and EDG-2-3'primer (5'TGC GGA GAG CTT TAA CCT CC-3', SEQ ID NO. 32), complementary to bases 1165 bp – 1184 bp with an amplification length of 348 bp of the EDG-2 cDNA (GenBank accession no. NM010336), the primer EDG-4-5'primer (5'-CCT ACC TCT TCC TCA TGT TC-3', SEQ ID No. 33), spanning bases 344 bp – 363 bp, and EDG-4-3'primer (5'-TAA AGG GTG GAG TCC ATC AG-3', SEQ ID No. 34), complementary to bases 1199 bp – 1148 bp of the EDG-4 cDNA (GenBank accession no. NM020028), the primer EDG-7-5'primer (5'-GGA ATT GCC TCT GCA ACA TCT-3', SEQ ID No. 35), spanning bases 673 bp – 693 bp, and EDG-7-3'primer (5'-GAG TAG ATG ATG GG TTC A-3', SEQ ID No. 36), complementary to bases 1096 bp – 1054 bp of the EDG-7 cDNA (GenBank accession no. NM022983). PCR was performed using a Thermo-cycler PTC-100 (MJ Research, Inc.) in 25 µl final volume containing 10 µmol/l dNTPs (Pharmacia, Germany), 2.5 units Taq Polymerase (Stratagen, Germany), 2.5 µl 10 x buffer including 2.5 mol/l $MgCl_2$ (Stratagen, Germany), 10 µmol/l of each primer, and 2 µl of each cDNA for all molecular analysis. For all EDG receptors, as well as for PRG-1 amplification, the cycle program was: 2 min at 95°C, 40 x (94°C, 30 sec; 52°C, 30 sec; and 72°C, 1 min), and 5 min at 72°C. Amplification of β-actin cDNA was performed as described by Bräuer et al. (2000) Hippocampus 10:632-644.

8. Immunocytochemical staining of rat hippocampus

The antibody described in experiment 6 was also used for the immunocytochemical staining and Western blot analysis. For Western blot analysis, rat adult and 5dal hippocampus extracts were separated on a 12% SDS/PAGE and electroblotted to nitrocellulose membranes (Millipore, Germany). All incubation was done overnight at 4°C in PBST. The PRG-1 antiserum was used at a 1:2000 dilution. Secondary anti-rabbit antibody coupled with horseradish peroxidase was used at a 1:5000 dilution, and visualized by incubation in

ECL detection reagents (Amersham Pharmacia, Germany). The protocol for the immunocytochemistry is essentially the same as described in detail in Bräuer et al., 2001 (FASEB J, 15, 2689-2701). The immunocytochemical staining of rat hippocampus revealed that PRG-1 was specifically expressed in neurons (see Fig. 7, panel A) and in particular pyramidal neurons are labeled in the CA1 and CA3 region, polymorphic cells are stained in the hilus and granule cells of the dentate gyrus are also immunopositive. However, the outer molecular layer, the termination zone of afferents from the entorhinal cortex (Skutella T. and Nitsch R. (2001) Trends. Neuroscience 24:107-163) showed no PRG-1 positive fibers (Fig. 7, panel A). Conversely five days after entorhinal cortex lesion, a clear immunoreactive PRG-1 positive band appeared in the denervated outer molecular layer (Fig. 7, panel B). Western blot analysis revealed a 50% increase in PRG-1 expression in the denervated hippocampus (Fig. 7, panel C). PRG-1 immunostaining highlighted single axonal processes in the outer molecular layer which form terminal branches (Fig. 8, panel A). The higher magnification of an area from the immuno stained axons showed that PRG-1 is indeed localized in the growth cone-like axon structures in the denervated zones of the hippocampus (see Fig. 8, panel B).

Subcellular localization

PRG-1 tagged with the eGFP reporter gene was used to identify the subcellular localization. Golgi apparatus was visualized with the cell tracker BODYPY ceramide (Molecular Probes, Oregon). The staining protocol was obtained from Molecular Probes.

9. Effect of PRG-1 expression on the LPA response of neurons

LPA induced neurite retraction in explants

Entorhinal explants from E16 and P0 rat pups were obtained from timed-pregnant Wistar rats and were cultivated as described (N. E. Savaskan (2000) Eur. I. Neurosci 12:1024-1032). In brief, entorhinal cortex was carefully dissected from the hippocampal anlage and the meninges were removed. Explants were gently transferred with a fire-polished Pasteur pipette into 12-well plates and cultivated on baked glass cover slides coated with laminin and poly-L-lysin (25 µg/ml and 10 µg/ml, respectively) in culture medium containing selenium-defined fetal bovine serum [5%] (N. E. Savaskan et al (2000) FASEB J. e-published) (Neurobasal medium plus 25 µg/ml Penicillin/Streptomycin; B-27 supplement). After 24 h, culture medium was exchanged and cultivation was further performed in serum-free

Neurobasalmedium for 20 h. Serum-starved explants were treated with 100 nmol/l oleoyl-LPA (5 mmol/l stock solution in ultra-filtrated water) for 10 min or with vehicle (0,9% NaCl) and then fixed in 4% paraformaldehyde for 20 min. For F-actin staining, fixed tissues were incubated with TRITC-phalloidin (0.1 µg/ml, Sigma, Germany) for 40 min, followed by incubation with HOECHST 33258 dye (1:20,000, Sigma, Germany) for 5 min at room temperature. After three washing steps in PBS, explants were coverslipped with ImmunoMount (Merck, Germany) prior to analysis. Images were taken with a CCD camera on an Olympus BX-50 microscope and quantification was performed using the Meta Morph analysis system (Universal Imaging, PA). For statistical analysis Statview II was used (Abacus, USA).

A dose response of LPA neurite length of E16 and P0 explants was done as described above, however, with 0, 0.1, 1.0 and 10 µmol/l.

Entorhinal explants obtained at day 16 (E16) do not express PRG-1 while postnatal explants (P0) express PRG-1(see Fig. 9, panel A). In contrast, the LPA-specific receptors EDG-2/4/7 were equally expressed in both embryonic and postnatal explants (see Fig. 9B). The control RT-PCR with β-actin showed the integrity of the RNA from E16 and P0 cells. Both embryonic and postnatal explants grow equally well under serum-free culture conditions and show long extending axons (see Fig. 9, panels D and F). However, their response to LPA differed dramatically (see Fig. 9, panels E and G). Whereas application of 100 nmol/l LPA led to rapid neurite retraction in embryonic entorhinal explants (E16; n = 20, compare panel D to panel E), postnatal explants (P0; n = 22, compare panel F to panel G) did not differ significantly from vehicle treated control cultures. Thus, postnatal entorhinal axons expressing PRG-1 are resistant to LPA-induced neurite retraction. The amount of retraction observed in panels D-G is quantified in Fig. 10, panel A. The dose response is shown in Fig. 10, panel B.

10. Differential effect of PRG-1 and PRG-1 mutant on LPA-induced neurite retraction

Site-directed mutagenesis of PRG-1$^{HIS/LYS}$

The rat PRG-1 full length clone was amplified by Marathon PCR (Clontech, USA) from adult rat hippocampus RNA (SEQ ID No. 17). For transfection studies, the full length PRG-1 coding sequence was fused to EGFP (pEGFP-N1 vector Clontech, USA). The

PRG-1$^{His/Lys}$ exchange mutant at the catalytic histidine (His-252) was introduced in the same protein fusion vector by site specific mutagenesis (CAT to AAG).

LPA induced neurite retraction and protection in N1E-115 cells

N1E-115 mouse neuroblastoma cells (ATCC: CRL-2263) were routinely grown in DMEM medium supplemented with selenium-defined fetal bovine serum (10%). The cells were seeded on baked glass cover slides at a density of 10,000 cells/cm^2. The next day, cells were transfected with the cationic lipids procedure (FuGene6, Roche, Germany) and cultivated for 24 h. Serum-starvation was performed for 20 h in DMEM medium, followed by treatment with 10 µmol/l oleoyl-LPA or vehicle (0.9% sodium chloride) (K. Jalink et al (1993) Cell Growth Differ. 4:247-255). After 10 min, cells were fixed in 4% paraformaldehyde for 20 min at room temperature and further analysis processed as described above. Images were taken with a CCD camera on an Olympus BX-50 microscope. Quantification was performed with the Meta Morph analysis system (University Imaging, PA). For statistical analysis Statview II was used (Abacus, USA). The effects of transfection on cell viability were analysed by MTT assay and propidium iodide staining (Savaskan N.E. et al. (2002) FASEB J. 17:112-114).

N1E-115 cells are uniformly sensitive to LPA-induced growth cone collapse (see Fig. 11 and compare first row of panels versus second row of panels). This is also confirmed by phalloidin staining (K. Jalink et al, (1994) J. Cell Biol. 126:801-810) which showed actin polymerization upon PRG-1 overexpression, however, led to a resistance of N1E-115 cells to LPA-induced growth cone collapse and also prevented LPA-induced actin-polymerization (see Fig. 11, third row of panels). The mutation of the conserved catalytic histidine (His-252) to a lysine (PRG-1$^{His/Lys}$) a change which has been shown to completely abolish enzymatic function of the catalytic center of LPP-1 (N. Zhang, et al. (1997) *supra*) no longer prevented LPA-induced retraction of processes as achieved by the wt-construct. This shows that the conserved enzymatic domain of the LPP-1 family is necessary for PRG-1 function in attenuating LPA-induced neurite retraction. The results of the experiments are quantified in Fig. 12, panel A. The transfection, however, had no effect on the expression of the LPA-receptors EDG-2/4//7 (see Fig. 12, panel B). The control for the integrity of the RNA tested by RT-PCR is shown in Fig. 12, panel C. The resistance against CPA-induced growth cone collapse achieved by PRG-1 overexpression could only be overcome by a 10-fold increase of LPA applied to the culture (Fig. 12, panel D).

11. Ectophosphatase activity in PRG-1 transfected N1H-115

The assay procedures used were adapted from those described in Imai et al. (2000) J. Clin. Endocrinol. Metab 85:3370-3375 and Hooks S.B. et al. (2001) J. Biol. Chem. 276:4611-4621. Briefly, transfected cells were harvested after serum-free cultivation for 20 h by scraping in lysis buffer (containing 20 mmol/l HEPES pH 7.4, 1 mmol/l $NaHCO_3$, 500 µmol/l DTT, 1 mmol/l EGTA) and sonicated with two strokes (Bandolin GM 70, Germany). After centrifugation at 800 x g, the supernatant was diluted in lysis buffer and centrifuged at 100,000 x g for 1 h. Alternatively, the supernatant was topped on a sucrose step gradient (50% and 5%) and centrifuged at 100,000 x g for 1 h (Savaskan, N.E. et al. (2000) Eur. J. Neurosci. 12:1024-1032. The resulting pellet and interphase, respectively, were re-homogenized and centrifuged again at 100,000 x g for 1 h. The crude membrane pellet was re-suspended in reaction buffer (50 mmol/l HEPES pH 7,5; 1 mmol/l EGTA) and protein concentration was determined spectroscopically by Bradford protein assay (Amersham, Germany). Assessment of LPA metabolism was performed with exogenous ^{3}H-oleoeyl-LPA (Perkin Elmer, Germany) measuring ^{3}H-oleoeyl-glycerol production. Briefly, 10-25 µg membrane proteins were pre-warmed to 37°C in reaction buffer and reactions were started by the addition of 10 µmol/l ^{3}H-oleoeyl-LPA. The reaction was allowed to proceed for 5-30 min at 37°C and stopped with the addition of 2.5 vol acidified methanol and 1.5 vol chloroform. After two-phase separation, the chloroform phase was dried under N_2 and applied to silica gel matrices (Machery Nagel, Germany). Plates were developed in chloroform-aceton-acetic acid (90:10:1). All fractions of dried plates were scintillation counted and compared with authentic standards (LPA, 1-monoolein, 1,2-monoolein, oleic acid). All experiments were performed in triplicate. The ecto-phosphatase assay in intact cells was determined as described above. ^{3}H-LPA was added to the serum-free medium and the reaction was allowed to proceed for 5-60 min. The reaction was stopped by adding 2.5 vol acidified methanol and 1.5 vol chloroform to the supernatant. The radioactivity was determined in the lipid fraction as described above.

The results from three independent sets of experiments are shown in Fig. 12, panel F (one set with n = 40 for each group in the outgrowth assay). PRG-1-eGFP showed essentially the same ecto-phosphatase activity as the wt PRG-1 construct. Statistical differences from controls are marked with an asterisk (mean $\pm$ S.D.), $***P < 0.001$; two-tailed t test with Bonferroni correction for multiple comparisons.

The extracellular LPA-degradation achieved by transfected N1E-115 cells revealed a 5-fold increase in ecto-phosphatase activity of wildetype PRG-1 transfectants when compared to eGFP transfection alone (Fig. 12, panel F). Moreover, point-mutation in the conserved catalytic domain by His/Lys exchange led to a 95 % decrease of ecto-phosphatase activity (Fig. 12, panel F). These findings show that PRG-1 has ecto-phosphatase activity which is conveyed by a conserved enzymatic domain present in the LPP-1 family, and necessary for attenuating LPA-induced neurite retraction. In addition transfection of the PRG-1 construct into N1E-115 cells did not prevent CPA-induced retraction of processes as achieved by the wt-constructs, whereas cell viability was unaffected (see Fig. 12, panel E).

Thus the ecto-phosphatase activity of PRG-1 was shown by two independent experiments: a) transfection of a mutant construct into N1E-115 cells did not prevent LPA-induced retraction of processes as achieved by transfection of wt construct and b) the transfection of the wt construct led to a 5-fold increase in ecto-phosphatase activity, if compared to cells transfected with a control vector.

12. Model of axon growth mechanism

Fig. 13 shows a diagram of the proposed axon growth mechanism in a phospholipid rich environment. Axons that are sensitive to repulsive phosphor lipid but do not express PRG-1 are unable to cross a phosphor lipid-rich barrier. In contrasts PRG-1 expressing neurons can grow through a phosphor lipid rich zone by local depleting the extracellular pool of repulsive phosphor lipids acting as ligands on EDG-receptors. This way, PRG-1 may regulate the activation of EDG-receptors and thereby modulate axonal outgrowth.

13. Northern blot analysis of PRG-3 expression

The full coding region of PRG-3 was amplified by PCR and the product was p32-dCTP labelled by T4 kinase reaction. Hybridization was performed overnight at 68°C and exposure followed for 20h. The multi-tissue Northern blot analysis of rat PRG-3 mRNA shows a single 2,4 kb band in brain and liver. Slightly lower bands are also present in kidney and testis as depicted in Fig. 15.

14. *In situ* hybridization analysis of PRG-3 expression

For hybridization, we used two antisense oligonucleotides which both gave essentially the same hybridization signal: 5'-GCA GAG GTC TGA ATT CTA GTG TCT ATC GTT ATA GTT CCT TAA CAG TGT GGG-3' (SEQ ID NO. 37) and 5'- CAT CCT TCT GTA GTA GCT TTC TGC CTC TGC CTC CAC TTC TCT CT -3' (SEQ ID NO. 38) complementary to rat PRG-3 sequence (SEQ ID NO. 23). The oligonucleotide was synthesized by Metabion (Munich, Germany). The specificity was confirmed by a BLAST GenBank search to rule out cross-hybridization with other genes. We used the protocol as previously described (Brauer et al., 2001, supra).

Kainate administration and assessments of seizure activity and neuronal cell death in vivo

Six rats, weighing 200-300 g, were weight-paired (± 10 g per pair). These animals received a single i.p. injection of kainic acid (10 mg/kg bodyweight; from Ocean Products Int., Canada) freshly dissolved in 0.9 % saline. Behavior was then observed constantly for 24 hr via video time lapse recordings. Controls received a single i.p. injection of saline in the same volume or were not treated . Severity of seizures was scored for 4 h after kainate injection using the classification of Zhang et al. Twenty-four hours after kainate injections, rats were killed and brains were harvested. Coronal brain sections were cut on a freezing microtome with 20 µm thickness and stained with cresyl violet and acid fuchsin. Nissl-positive undamaged neurons were counted in five coronal brain sections per animal (sections were chosen by unbiased sampling), and the mean number of cells per section were determined such that the value obtained for each rat represents an average total number of neurons counted per section (250 µm by 250 µm square in the middle of the CA1 region). Counts were performed by an investigator blind to treatment status.

The hybridization was carried out as described above. At embryonic day 16 (E16) a hybridization signal for PRG-3 can be detected in the hippocampal anlage, thalamus, and in the olfactory bulb. At perinatal stages (E20 – P0), a strong hybridization signal is found in the cortex and hippocampus except the dentate gyrus (dg). Fig. 15, panel B shows a higher magnification of the hippocampus. Note that in the dentate gyrus the first hybridization signal occurs at postnatal day ß (P0). Fig. 15, panel C shows that adult, PRG-3 transcripts can be found in all principal layers of the hippocampus. A rapid PRG-3 repression is found six hours after kainic acid application. Five days after kainic acid application, PRG-3 mRNA shows comparable levels to the adult non-treated controls. CA, cornu ammonis; cb,

cerebellum; Cx, cortex; dg, dentate gyrus; KA, kainic acid. Scale bar in A, is 1.8 mm and in B, 400 µm.

15. Effect of PRG-3 expression on neurons

N1E-115 cells were transfected with peGFP-N1 reporter vector alone or with a pPRG-3-eGFP fusion construct as descried above. As can be seen from the second and third row the eGFP is mainly found in the cytosol whereas PRG-3-eGFP is localized in the plasma membrane and in neurite extensions (arrows). Note that PRG-3-eGFP expression induce a spreading-like phenotype and long extensions. Scale bar in the second row of panels represents 2 µm; in the third row of panels 5 µm.

16. PRGs as a prognostic marker for cancer

To test the hypothesis, that PRG-1 might be a prognostic marker for cancer diagnostics, differential human prostatic tumors were screened by means of PCR and immunocytochemistry. Adenocarcinoma is the most malignant neoplasia of human males in western world. Samples from 10 matched pairs of microdissected prostate tissue (tumor and normal) were frozen and sections were made. A transcription analysis was performed using RNA preparations from these samples. It was found, that in normal prostate tissue almost no PRG-1 transcript or protein could be detected. In tumor tissue with Gleason tumor grades 1-3, which is characterized as low-grade tumors, we found only 2 PRG-1 positive samples. Analysis of high-grade tumors (Gleason grade 4-5) revealed in 80% of the cases a significant PRG-1 upregulation. Therefore, PRG-1 is an independent prognostic marker for high-grade prostate tumors in human males.

17. PRG as a prognostic marker for Alzheimer's disease

Alzheimer's disease is characterized by intracellular neurofibrillary tangle formation formed by tau-based paired helical filaments (PHF) and by extracellular beta-amyloid plaques. The degree of Alzheimer dementia correlates well with the severity of PHF occurrence. These PHF are formed by hyperphosphorylated tau formation. Analysis of brain sections from patients with Alzheimer's disease revealed a reduced PRG-1 expression. To gain insights into the functional role of PRG-1 in Alzheimer's pathology we used an established cell culture model.

Comparing neurons overexpressing PRG-1 with control transfected cells revealed an significant reduction of hyperphosphorylated tau protein. Also, using okadaic acid or LPA as known tau hyperphosphorylation induced substances, we found a significantly decrease in hyperphosphorylated tau and PHF formation.